

# SEQUENCE ALIGNMENT -

## SEQ ID NO: 1 VS SEQ ID NO: 3

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 5, 2003, 11:43:46 ; Search time 20 Seconds  
(without alignments)  
4.028 Million cell updates/sec

Title: us-10-090-516-3  
Perfect score: 4875  
Sequence: 1 atggacgtgaaggagaggaa.....ctactgggatgcccctctga 4875

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.0

Searched: 1 seqs, 8262 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database : us-10-090-516-1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4874	100.0	8262	1	us-10-090-516-1	

### ALIGNMENTS

RESULT 1  
us-10-090-516-1

Query Match 100.0%; Score 4874; DB 1; Length 8262;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4874; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC	60
Db	1	ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC	60
Qy	61	CGCTACACCAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCGAGAAATCGTACAGC	120
Db	61	CGCTACACCAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCGAGAAATCGTACAGC	120
Qy	121	TCCAGCGAGACCCCTGAAGGCTACGACAGGACGCCCGCTAGCCTATGGCAGCCGCGTC	180
Db	121	TCCAGCGAGACCCCTGAAGGCTACGACAGGACGCCCGCTAGCCTATGGCAGCCGCGTC	180
Qy	181	AAGGACATTGTGCCGAGGAGGCCGAGGAATTCTGCCGACAGGTGCCAACTTCACCCTG	240
Db	181	AAGGACATTGTGCCGAGGAGGCCGAGGAATTCTGCCGACAGGTGCCAACTTCACCCTG	240
Qy	241	CGGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCCTGTACCGGACAGACATT	300

Db 241 CGGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCTGTACCGGACAGACATT 300  
 Qy 301 GGCCTCCCCCACTGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360  
 Db 301 GGCCTCCCCCACTGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360  
 Qy 361 ACGGTGCTGTCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 420  
 Db 361 ACGGTGCTGTCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 420  
 Qy 421 AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480  
 Db 421 AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480  
 Qy 481 AACACTGAGACTGATCATCCGGGCGGCCTGCAGAACACGCGCGGCTCCGGACGCGCGCG 540  
 Db 481 AACACTGAGACTGATCATCCGGGCGGCCTGCAGAACACGCGCGGCTCCGGACGCGCGCG 540  
 Qy 541 CCGCCGCTCTCGCACGCCCACACCCCAACCAGCACCACGCGGCCTCCATTAACCTCCCTG 600  
 Db 541 CCGCCGCTCTCGCACGCCCACACCCCAACCAGCACCACGCGGCCTCCATTAACCTCCCTG 600  
 Qy 601 AACCAGGGGCAACTTCACGCCGAGGAGCAACCCAGCCCGGCCCCACGGACCACTCGCTC 660  
 Db 601 AACCAGGGGCAACTTCACGCCGAGGAGCAACCCAGCCCGGCCCCACGGACCACTCGCTC 660  
 Qy 661 TCCGGAGAGCCCCCTGCCGCGGCGCCAGGAGCCTGCCACGCCAGGAGAACTGGCTG 720  
 Db 661 TCCGGAGAGCCCCCTGCCGCGGCGCCAGGAGCCTGCCACGCCAGGAGAACTGGCTG 720  
 Qy 721 CTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCCATTCTTAGGGACA 780  
 Db 721 CTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCCATTCTTAGGGACA 780  
 Qy 781 TTGCAGGACAACCTCATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGGCTTAC 840  
 Db 781 TTGCAGGACAACCTCATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGGCTTAC 840  
 Qy 841 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCCGCTCTTCTGCACCACATCA 900  
 Db 841 AGTGACGGGCACTTCCTCTTCAAGCCTGGAGGCACCTCCCCGCTCTTCTGCACCACATCA 900  
 Qy 901 CCAGGGTACCACTGACGTCCAGCACAGTGTACTCTCCTCCGCCCGACCCCTGCCCGC 960  
 Db 901 CCAGGGTACCACTGACGTCCAGCACAGTGTACTCTCCTCCGCCCGACCCCTGCCCGC 960  
 Qy 961 AGCACCTTCGCCCCGCGGCGCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAAGTGAAG 1020  
 Db 961 AGCACCTTCGCCCCGCGGCGCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAAGTGAAG 1020  
 Qy 1021 TGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGTGGCATACTTT 1080  
 Db 1021 TGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGTGGCATACTTT 1080  
 Qy 1081 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGAGATGTAT 1140  
 Db 1081 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGAGATGTAT 1140  
 Qy 1141 GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCAGCGTCTCCCTATACCCC 1200  
 Db 1141 GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCAGCGTCTCCCTATACCCC 1200  
 Qy 1201 TCAGGGGGCACTGGCTTAGAGACCCTGACAGGAAAGGCAAAGGAACCAGAAAGGAAAG 1260  
 Db 1201 TCAGGGGGCACTGGCTTAGAGACCCTGACAGGAAAGGCAAAGGAACCAGAAAGGAAAG 1260  
 Qy 1261 CCCAGTAGTTTCTTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG 1320  
 Db 1261 CCCAGTAGTTTCTTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG 1320  
 Qy 1321 CGAGCTTCCAGAAGATTCTCTGGCACTTTCTGGAGATCTCAAGTGTTCATAGACCAT 1380

Db	1321	CGAGCTTCCCAGAAGATTCCCTCCTGGCACTTCTGGAGATCTCAAGTGTTTCATAGACCAT	1380
Qy	1381	CCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTATGGC	1440
Db	1381	CCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTATGGC	1440
Qy	1441	AGAAAAGGCCTCCCTCCTTCACATACACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGG	1500
Db	1441	AGAAAAGGCCTCCCTCCTTCACATACACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGG	1500
Qy	1501	AGGCTCCTAACCCAGGAGGCGCGGAGCCTAGAGGGGACCCGCGCCAGTCTCGGGGAACT	1560
Db	1501	AGGCTCCTAACCCAGGAGGCGCGGAGCCTAGAGGGGACCCGCGCCAGTCTCGGGGAACT	1560
Qy	1561	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTGGATTAGGAATCTGGCAC	1620
Db	1561	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTGGATTAGGAATCTGGCAC	1620
Qy	1621	TTGGCTTTTACAATGACGAAAGGAGTCAGAAGTGGTTTCCTTTCTCACCCTGCCATT	1680
Db	1621	TTGGCTTTTACAATGACGAAAGGAGTCAGAAGTGGTTTCCTTTCTCACCCTGCCATT	1680
Qy	1681	GAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCTCTGGGACC	1740
Db	1681	GAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCTCTGGGACC	1740
Qy	1741	TGCCACTGCTTCCTGGGTTTCCTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCCGTGCTC	1800
Db	1741	TGCCACTGCTTCCTGGGTTTCCTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCCGTGCTC	1800
Qy	1801	TGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGC	1860
Db	1801	TGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGC	1860
Qy	1861	GCTGAGTGCATGTGCCCCACCAACCAGTGTATCGATGTGGCCTGCAGCAACCATGGCACC	1920
Db	1861	GCTGAGTGCATGTGCCCCACCAACCAGTGTATCGATGTGGCCTGCAGCAACCATGGCACC	1920
Qy	1921	TGCATCACGGGCACCTGCATCTGCAACCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTG	1980
Db	1921	TGCATCACGGGCACCTGCATCTGCAACCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTG	1980
Qy	1981	GACTGCATGGACCCACATGTTTCAAGCCGGGGTGTCTGCGTGAGAGGCGAATGCCACTGC	2040
Db	1981	GACTGCATGGACCCACATGTTTCAAGCCGGGGTGTCTGCGTGAGAGGCGAATGCCACTGC	2040
Qy	2041	TCTGTGGGATGGGGAGGCACCAACTGCGAGACCCCGAGGCCACATGCTTAGACCAGTGT	2100
Db	2041	TCTGTGGGATGGGGAGGCACCAACTGCGAGACCCCGAGGCCACATGCTTAGACCAGTGT	2100
Qy	2101	TCAGGCCACGGAACCTTCCTCCCGGACACCGGGCTTTGAGCTGTGACCCAAGCTGGACT	2160
Db	2101	TCAGGCCACGGAACCTTCCTCCCGGACACCGGGCTTTGAGCTGTGACCCAAGCTGGACT	2160
Qy	2161	GGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTA	2220
Db	2161	GGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTA	2220
Qy	2221	GGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCAGCCTGCGACCAGCGGGCCTGC	2280
Db	2221	GGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCAGCCTGCGACCAGCGGGCCTGC	2280
Qy	2281	CACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGGCAAGTGCAGTGCAGCCCTGGC	2340
Db	2281	CACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGGCAAGTGCAGTGCAGCCCTGGC	2340
Qy	2341	TGGAATGGCGAACACTGCACCATCGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGA	2400
Db	2341	TGGAATGGCGAACACTGCACCATCGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGA	2400

Qy	2401	TGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGC	2460
Db	2401	TGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGC	2460
Qy	2461	TGTGACACTTCCATGGAGACTGCCTGCGGTGACAGCAAAGACAATGATGGAGATGGCCTG	2520
Db	2461	TGTGACACTTCCATGGAGACTGCCTGCGGTGACAGCAAAGACAATGATGGAGATGGCCTG	2520
Qy	2521	GTGGACTGCATGGACCCTGACTGCTGCCTCCAGCCCCTGTGCCATATCAACCCGCTGTGC	2580
Db	2521	GTGGACTGCATGGACCCTGACTGCTGCCTCCAGCCCCTGTGCCATATCAACCCGCTGTGC	2580
Qy	2581	CTTGGCTCCCTAACCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTACAGCAG	2640
Db	2581	CTTGGCTCCCTAACCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTACAGCAG	2640
Qy	2641	AACCTACACTCCTTCTATGACCGCATCAAGTTCCTCGTGGGCAGGGACAGCACGCACATA	2700
Db	2641	AACCTACACTCCTTCTATGACCGCATCAAGTTCCTCGTGGGCAGGGACAGCACGCACATA	2700
Qy	2701	ATCCCCGGGGAGAACCCTTTGATGGAGGGCATGCTTGTGTATTTCGTGGCCAAGTGATG	2760
Db	2701	ATCCCCGGGGAGAACCCTTTGATGGAGGGCATGCTTGTGTATTTCGTGGCCAAGTGATG	2760
Qy	2761	ACATCAGATGGAACCCCCCTGGTTGGTGTGAACATCAGTTTGTCAATAACCCTCTCTTT	2820
Db	2761	ACATCAGATGGAACCCCCCTGGTTGGTGTGAACATCAGTTTGTCAATAACCCTCTCTTT	2820
Qy	2821	GGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCC	2880
Db	2821	GGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCC	2880
Qy	2881	ATCATCCTGCGGTTGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGGCTGCCA	2940
Db	2881	ATCATCCTGCGGTTGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGGCTGCCA	2940
Qy	2941	TGGGATCGCTTCTTTGTATGGAACCATCATCATGAGACATGAGGAGAATGAGATTCCC	3000
Db	2941	TGGGATCGCTTCTTTGTATGGAACCATCATCATGAGACATGAGGAGAATGAGATTCCC	3000
Qy	3001	AGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACG	3060
Db	3001	AGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACG	3060
Qy	3061	TCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCATTTGTGCCGAAATTCAGGCTTTGCAG	3120
Db	3061	TCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCATTTGTGCCGAAATTCAGGCTTTGCAG	3120
Qy	3121	GAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGACCCCT	3180
Db	3121	GAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGACCCCT	3180
Qy	3181	GGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCCTTCAACCTCATG	3240
Db	3181	GGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCCTTCAACCTCATG	3240
Qy	3241	AAGGTGCACCTCATGGTAGCGGTGGAGGGCGCCTCTTCAGGAAGTGGTTCGCTGCAGCC	3300
Db	3241	AAGGTGCACCTCATGGTAGCGGTGGAGGGCGCCTCTTCAGGAAGTGGTTCGCTGCAGCC	3300
Qy	3301	CCAGACCTGTCCTATTATTTCATTGGGACAAGACAGACGTCTACAACCAGAAGGTGTTT	3360
Db	3301	CCAGACCTGTCCTATTATTTCATTGGGACAAGACAGACGTCTACAACCAGAAGGTGTTT	3360
Qy	3361	GGGCTTTTCTAGAAGCCTTTGTTTCCGTGGGTATGAATATGAATCCTGCCAGATCTAATC	3420
Db	3361	GGGCTTTTCTAGAAGCCTTTGTTTCCGTGGGTATGAATATGAATCCTGCCAGATCTAATC	3420
Qy	3421	CTGTGGGAAAAAAGAACAACAGTGCTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGGA	3480
Db	3421	CTGTGGGAAAAAAGAACAACAGTGCTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGGA	3480

Qy	3481	GGATGGAGCCTAGACAAACATCATGCCCTCAACATTCAAAGTGGCATCCTGCACAAAGGG	3540
Db	3481	GGATGGAGCCTAGACAAACATCATGCCCTCAACATTCAAAGTGGCATCCTGCACAAAGGG	3540
Qy	3541	AATGGGGAGAACCAGTTTGTGTCTCAGCAGCCTCCTGTCTATTGGGAGCATCATGGGCAAT	3600
Db	3541	AATGGGGAGAACCAGTTTGTGTCTCAGCAGCCTCCTGTCTATTGGGAGCATCATGGGCAAT	3600
Qy	3601	GGGCGCCGGAGAAGCATCTCTGCCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTC	3660
Db	3601	GGGCGCCGGAGAAGCATCTCTGCCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTC	3660
Qy	3661	CTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAAC	3720
Db	3661	CTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAAC	3720
Qy	3721	TACATTAGAAGGATCTTCCCCTCTGGAAATGTCAACACATCCTAGAGCTGAGTCACAGT	3780
Db	3721	TACATTAGAAGGATCTTCCCCTCTGGAAATGTCAACACATCCTAGAGCTGAGTCACAGT	3780
Qy	3781	CCAGCACACAAATACTACCTGGCCACAGACCCCATGAGTGGGGCCGTCTTCCTTTCTGAC	3840
Db	3781	CCAGCACACAAATACTACCTGGCCACAGACCCCATGAGTGGGGCCGTCTTCCTTTCTGAC	3840
Qy	3841	AGCAACAGCCGGCGGGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAG	3900
Db	3841	AGCAACAGCCGGCGGGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAG	3900
Qy	3901	AACCTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCTCCCCTTTGATGACACTCGCTGC	3960
Db	3901	AACCTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCTCCCCTTTGATGACACTCGCTGC	3960
Qy	3961	GGGGATGGTGGGAAGGCCACAGAAGCCCACTCACCAATCCCAGGGGCATTACAGTGGAC	4020
Db	3961	GGGGATGGTGGGAAGGCCACAGAAGCCCACTCACCAATCCCAGGGGCATTACAGTGGAC	4020
Qy	4021	AAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAATGGG	4080
Db	4021	AAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAATGGG	4080
Qy	4081	ATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCGGCCACTCAGCTGTGAT	4140
Db	4081	ATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCGGCCACTCAGCTGTGAT	4140
Qy	4141	TCTGTATGGATATTTCCAGGTTACCTGGAGTGGCCACAGACTTAGCCATCAACCCA	4200
Db	4141	TCTGTATGGATATTTCCAGGTTACCTGGAGTGGCCACAGACTTAGCCATCAACCCA	4200
Qy	4201	ATGGACAACCTACTTTATGTCTCGACAACAATGTGGTCTGCAAACTCTGAAAACCCAC	4260
Db	4201	ATGGACAACCTACTTTATGTCTCGACAACAATGTGGTCTGCAAACTCTGAAAACCCAC	4260
Qy	4261	CAGGTGCGCATTGTGCGCGGGAGGCCCATGCACTGCCAGGTCCCTGGCATTGACCACTTC	4320
Db	4261	CAGGTGCGCATTGTGCGCGGGAGGCCCATGCACTGCCAGGTCCCTGGCATTGACCACTTC	4320
Qy	4321	CTGCTAAGCAAGGTGGCCATCCACGCAACCCTGGAGTCAGCCACCGCTTTGGCTGTTTCA	4380
Db	4321	CTGCTAAGCAAGGTGGCCATCCACGCAACCCTGGAGTCAGCCACCGCTTTGGCTGTTTCA	4380
Qy	4381	CACAATGGGGTCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAG	4440
Db	4381	CACAATGGGGTCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAG	4440
Qy	4441	GTCACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAA	4500
Db	4441	GTCACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGCCCCCAGTGGCTGTGACTGTAAA	4500
Qy	4501	AATGATGCCAACTGTGATTGTTTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAGTTA	4560

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Db 4501 AATGATGCCAACTGTGATTGTTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAGTTA 4560
Qy 4561 AATACCCCATCTTCCTTGGCTGTGTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGG 4620
      |||
Db 4561 AATACCCCATCTTCCTTGGCTGTGTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGG 4620
      |||
Qy 4621 AACATCCGAATTCGGTTTATCCGGAAGAACAAGCCTTTCCTCAACACCCAGAACATGTAT 4680
      |||
Db 4621 AACATCCGAATTCGGTTTATCCGGAAGAACAAGCCTTTCCTCAACACCCAGAACATGTAT 4680
      |||
Qy 4681 GAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGATACCACCGGCAAGCACCTG 4740
      |||
Db 4681 GAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGATACCACCGGCAAGCACCTG 4740
      |||
Qy 4741 TACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAACCTCACCTACACTGGGGACGGC 4800
      |||
Db 4741 TACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAACCTCACCTACACTGGGGACGGC 4800
      |||
Qy 4801 GACATCACACTCATCACAGACAACAATGGCAACATGGTAAATGTCCGCCGAGACTCTACT 4860
      |||
Db 4801 GACATCACACTCATCACAGACAACAATGGCAACATGGTAAATGTCCGCCGAGACTCTACT 4860
      |||
Qy 4861 GGGATGCCCCCTCTGA 4874
      |||
Db 4861 GGGATGCCCCCTCTGA 4874

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Search completed: May 5, 2003, 11:44:07  
Job time : 21 secs

Paper copy of sequence listing indicates  
SEQ ID NO:3 has "A" @ position 4875  
and SEQ ID NO:1 has "G" @ position  
4876. These nucleotides have been  
inserted for clarity.